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Five-year experience of vertebral osteomyelitis treatment at Kameda Medical Center, Japan

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Background: Vertebral osteomyelitis (VO) is caused by various pathogens. Although identifying the causative organism before starting the treatment is important, it is not always possible, thus empirical treatment is sometimes necessary.

Methods: We collected the clinical information of 76 patients with VO for the past five years from our electronic medical record system. Causative pathogen, mode of detection, site of infection, treatment duration, and outcome were reviewed retrospectively. In addition, we categorized all the patients into three groups: community acquired (CAVO), healthcare-associated (HCAVO), and hospital-acquired (HAVO), and evaluated the differences in the organisms.

Results: VO was clinically diagnosed in 76 patients. Causative organism was detected in 56 (73.6%). Most organisms were pyogenic except for one case of tuberculosis. Of these 55 patients, 18 (32.7%) had *Staphylococcus aureus* (12 methicillin-susceptible *Staphylococcus aureus* [MSSA] and 6 methicillin-resistant *Staphylococcus aureus* [MRSA]); 5 (9.1%) Coagulase-Negative Staphylococci (CNS); 7 (12.7%) β-Streptococci; 8 (14.5%) α-Streptococci; 9 (16.4%) Enterobactericiae; 3 (5.5%) Candida spp.; and 5 (9.1%) others. In 48 (87.2%) of the 55 patients with organism-proven VO, organisms were detected by blood culture. Twenty-eight (58.3%) of the 48 patients had persistent bacteremia, which is often seen with CNS and *S. aureus*. Infective endocarditis was confirmed in 9 (12.2%) patients. Biopsy was performed in 30 (40.5%) patients and organisms were cultured in 16 (53.3%) patients. Thirty-five (47.3%) patients were regarded as CAVO, 16 (21.6%) HCAVO, and 23 (31.1%) HAVO. Common organisms for CAVO were MSSA (26.0%), β-Streptococci (26.0%), and α-Streptococci (22.2%). Neither MRSA nor Candida spp. caused CAVO. Lower lumbar vertebrae were the most frequently infected area. Average duration of parenteral antibiotic treatment was 49 days. Thirty-eight (50%) patients were followed for at least half a year and only 2 (5.2%) patients were suspected to have relapsed.

Conclusion: Patients with VO are likely to have bacteremia; thus, blood culture is a useful tool to find the causative organism. If empirical treatment is necessary, it should be tailored according to the type of VO and local epidemiological data.

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Bacteraemia caused by genus Oligella

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Background: The Department of Medical Microbiology, Lillehammer has around 420 000 analyses yearly. We cover the counties of Oppland and Hedmark, analysing specimens from hospitals as well as from general practitioners and others. The counties of Oppland and Hedmark are located – bordering each other - in the Central Eastern part of Norway. The area of our counties equals 53 200 square kilometres i.e. approx. that of Denmark (43 094 square kilometres). The population is 371 500 (data as of the end of 2010).

Genus Oligella comprises small, non-fermentative, non-motile, non-sporeforming Gram-negative rods. Oligella comprises two species, namely **Oligella urethralis**, formerly **Moraxella urethralis** and **Oligella ureolytica**, formerly CDC group IVe. Moraxella urethralis has most frequently been associated with urinary tract infections. In MEDLINE (as of September 29, 2011) there were 26 "hits" when it comes to peer-reviewed articles concerning "Oligella" and two for Oligella and sepsis. We here describe what may be the first documented Norwegian case of bacteraemia caused by Oligella.

Methods: An 81 year old male was admitted to Sykehuset Innlandet Hospital in April 2011. From blood cultures, taken on admission, Gram-negative rod-shaped bacteria were grown on blood and chocolate agar. NIPH - performed reference testing, including 16SrRNA sequencing.

Results: Growth conditions etc.
Haemolysis: None
Growth – blood agar - aerobic conditions: 3+
Growth – chocolate agar - aerobic conditions: 3+
Growth – lactose agar - aerobic conditions: None
Corrosion: Negative
Motility 22 deg. C None
Motility 30 deg. C None
Biochemical and other reactions:
Mannitol: Negative
Nitrate reduction: Negative
Catalase: Positive
Oxydase: Positive
OF Glucose: No growth
Susceptibility:
Vancomycin 5 ug: Resistant

Sequencing: A 524 base pair fragment of the 16SrRNA gene was sequenced. It showed 99% homology with *Oligella urethralis*, hence the bacterium belongs to genus Oligella.

Conclusion: Previously our department has detected cultures positive for Anaerobiospririllum succiniciproducens, Dialister sporosintes, Granulicatella adjacens, Actinobaculum schalii, Clostridium scindens, Globicatella sulphidifaciens, Eggertella lenta, Leptotrichia trevisianii, Weeksella virosa and Bulleidia moorei – among others. A medium-sized laboratory often does not have the equipment to perform more sophisticated analyses. Therefore some samples must be referred to central reference laboratories.

This case report demonstrates the importance of co-operation between laboratories on a regional and a central level.

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A survey on community acquired-meticillin resistant *Staphylococcus aureus* burden among university students

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Background: The present study was conducted to survey the prevalence of community acquired-methicillin resistant *Staphylococcus aureus* (CA MRSA) among healthy university students.

Methods: Specimens were collected from skin surface, nostrils, upper throat, scars or pimples from student volunteers. Swabs was inoculated on mannitol salt agar and potential *Staphylococcus aureus* cultures were isolated and identified further using microbiological and biochemical characteristics. Antibiotic susceptibility was confirmed particularly resistance to oxacillin resistances and other antibiotics. PCR was performed to detect the presence of SCCmec and *pvl* genes in CA-MRSA isolates.

Results: Eighty five students volunteered in the study with 340 specimens were collected. Fifty five students were highly involved in sport activities and 30 were not involved in sport activities. *S. aureus* was isolated from 85 specimens but only 25 were confirmed to be oxacillin resistant thus considered as CA-MRSA. Seventeen (68%) were from the skin surfaces and 11 from wound specimens. No difference between CA-MRSA and *S aureus* ATCC 25923 in basic microbiological and biochemical observations. The CA-MRSA isolates were resistant to beta lactam antibiotic such as penicillin (100%) and ampicillin (23%) as well as non-beta lactam antibiotics such as fusidic acid (55%), mupirocin (60%) and vancomycin (25%). In PCR, all the isolates were detected for *SCCmec* gene. The *pvl* gene was detected in 10 (40%) isolates. One isolate that showed the presence of all genes was from the skin specimen collected from a female student not highly involved in sport activities, did not share personal equipments with other students and she had never received treatment from hospitals.

Conclusion: CA-MRSA colonization in healthy university students was low with only 7.3% of the isolates were detected as CA-MRSA. However, vancomycin resistant isolates detected in 25% of the CA-MRSA isolates should be noted and be aware of. The changing epidemiology of MRSA and preventive measures are needed to avoid outbreaks.

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Prevalence of serotypes and molecular types among *Streptococcus pneumoniae* isolates causing invasive disease in Singapore between June 2009 and August 2010

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Background: *Streptococcus pneumoniae* is a major cause of sepsis, meningitis and respiratory disease worldwide. World Health Organisation (WHO) reports that between 700,000 and 1 million children aged less than 5 die from pneumococcal infections. There are three pneumococcal conjugate vaccines (PCVs) that consist of 7, 10 or 13 of the most common capsular polysaccharides available for children. However, pneumococcal populations have been observed to undergo temporal changes in clonal distribution when the pressure from a vaccine is present. Therefore, the understanding of the underlying population structure is informative for formulating vaccine policy. We present epidemiological data on IPD from the national surveillance scheme in Singapore.

Methods: One hundred fifty-four IPD isolates (children <5 years: n = 11, children [5-18) years: n = 2, adults [18-64) years: n = 77, adults >64: n = 64), received by the National Public Health Laboratory in Singapore from June 2009 to August 2010, were characterised using serotyping and MLST.

Results: Commonly occurring serotypes (in rank order) were: 6B, 19A and 19F in children <5 years; 19A, 7F, 3 and 8 in adults aged 18-64, and 3, 19A and 14 in adults over 64 years old. Two isolates from children aged 5-18 years were 4 and 23F. The 7-valent pneumococcal conjugate vaccine (PCV7) could prevent 38% of IPD, whereas PCV10 and PCV13 could prevent 50% and 62% of IPD respectively. Comparative eBURST showed that 16 STs were singletons and 13 of them were new STs. The most common clones ST9, ST81 and ST320 were found in all age groups (with exception for children aged 5 to 18 years). Serotypes 3, 19F and 23F contained the most of the new STs.

Conclusion: The serotype distribution reported here suggests that PCV would be effective in reducing pneumococcal disease burden in Singapore. Although PCVs would target the majority of common serotypes, differences in the clonal composition are important to consider because of the ability of pneumococcus to switch capsule types through mutation and recombination. Considerable genetic diversity among Singaporean IPD isolates was reported, providing a reservoir for genetic exchange. Further studies to analyse pneumococci in the region are warranted.

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